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Zea mays DNA fragm
Zea mays DNA fragm
Plant microsatelli
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Plant microsatelli

Zea mays DNA fragm Plant microsatelli Plant microsatelli Fusarium venenatum

AAH33084 AAT62711 AAT62712 AAT62722 AAX29692 AAT62712 AAX62712 AAX62712 AAX6272694 AAT62726

Human hypusine pro
DNA from construct
Dictyostelium hypu
DNA from construct
DNA from construct
DNA from construct

DNA from construct DNA from construct DNA from construct colon cancer

BP.

ALIGNMENTS

AAD02349 AAQ23739 AAC43649

Aspergillus oryzae Yeast hypusine pro Arabidopsis thalia Plant microsatelli Human polynucleoti Human polynucleoti Human RNA metaboli Cycloheximide sens Zea mays DNA fragm

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Copyright (c) 1993 - 2000 Compugen
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WPI; 2001-061978/07. P-PSDB; AAB66877. 06-JUL-1999; 99US-0348675. 19-JUN-2000; 2000US-0597771. 06-JUL-2000; 2000WO-US18364. 11-JAN-2001. WO200102592-A2 Lycopersicon sp. Tomato; eIF-5A; eukaryotic initiation factor 5A; senescence inhibition; 10-APR-2001 (SENE-) SENESCO INC. eIF-5A coding sequence. JE, (first entry) Wang T, Ę

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Best Local Similarity
Matches 380; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tomato, Arabidopsis and carnation cDNA clones encoding senescence-induced deoxylypusine synthase and eIF-5a, useful inhibiting senescence in a plant when introduced in reverse
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P-PSDB; AAB66878.
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19-JUN-2000; 2000US-0597771.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 5; Fig 14; 135pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-JUL-2000; 2000WO-US18364
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                                                                                         cctcaaaaactttcccacagcaagctggaaccatccgtaagaatggttacatcgttatca
                                                                                                                                            ctagagagagaagcatgtcggacgaagaacaccattttgagtcaaaaggcagatgctggtg
                                                                           catccaagacttaccctcaacaagctggtacaatccgcaagagcggtcacatcgtcatca
                                                                                                                              cgaaaaatcgaacgatgtcggacgatcaccatttcgagtcatcggccgacgccggag
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76.5%;
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                                                                                                                                                                                               Score 309.8;
Pred. No. 2.1
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2.1e-71;
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PRRRPRRRPRRRPRRRPRRRPRRRPRRRPRRRPRRRPR	Qy Db	Qy Db	ОУ ОУ ОУ ОУ
RESULT 3  ACC39165 standard; DNA; 768 BP.  XX ACC39165;  XX Hybridisation assay; genetic mapping; gene expression control; Protein identification; signal transduction pathway; metabolic; ACC 2cam mays DNA fragment SPQ ID NO: 23616.  XX Hybridisation assay; genetic mapping; gene expression control; Protein identification; signal transduction pathway; metabolic; ACC 2cam mays subsp. mays.  XX Deal mays subsp. mays.  XX Expression control; Protein identification; signal transduction pathway; metabolic; ACC 2cam mays subsp. mays.  XX Expression.  XX Expression.  XX Expression control; Protein identification; Spq. 121625.  XX Expression.  XX 25-FEB-1999; 99US-0121825.  XX 25-FEB-1999; 99US-0121825.  XX 25-FEB-1999; 99US-0121825.  XX 25-FEB-1999; 99US-0121826.  XX 25-FEB-1999; 99US-0121826.  XX 25-FEB-1999; 99US-0121821.  XX 25-FEB-1990; 99US-0121821.  XX 25-FEB	ccaagaattag 525          gtggcaagtag 549	cttcctgctgargaggcccttgtgaagcagatgaaggaggatttgaagcttgtgaggcagatggaggaggaggagatttgaagcctgtgtggtgtgtgggcgaagagaggagattaacgcc 	
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990S - 0.139459 990S - 0.139459 990S - 0.139460 990S - 0.139461 990S - 0.139461 990S - 0.139463 990S - 0.139750 990S - 0.139819 990S - 0.140654 990S - 0.141842 990S - 0.142055 990S - 0.142054 990S - 0.142977 990S - 0.142977 990S - 0.144005 990S - 0.142977 990S - 0.144005 990S - 0.144005 990S - 0.142977 990S - 0.144005 990S - 0.145008 990S - 0.145008 990S - 0.145218 990S - 0.145218 990S - 0.145218 990S - 0.145218 990S - 0.145218	9US-0139492 9US-0139454 9US-0139455 9US-0139456	905-01 905-01 905-01	905-01 905-01 905-01 905-01 905-01 905-01 905-01

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RRESULT
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XX AAF3
AC AAF3
XX AAF3
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DT 10-A
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COMMENT
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Best Local Similarity
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29-OCT-1999
                                        06-JUL-1999; 99US-0348675.
19-JUN-2000; 2000US-0597771.
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                                                                                                                                                                                                                            Arabidopsis sp.
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  (SENE-) SENESCO INC
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milarity 77.2%;
Conservative
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990S-0161360.
990S-0161361.
990S-0161920.
990S-0161992.
990S-0161993.
990S-0162142.
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Pred. No. 2e-70;
0; Mismatches 110;
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מה סיסים סלים סיסים סיסים סיסים סיסים סיטים סיטי

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RESULT
AAC46522
ID AAC4
XX
AC AAC4
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Best Local Similarity 77.8
Matches 374; Conservative
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                                      AAC46522 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 702 BP; 186
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on; signal transduction pathway;
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01-JUN-1999;
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                                                                                                                                                                 and associated flanking species. The sequences comprise a central core repeat sequence, especially selected from the sequences AAA32094-A32096 with left and right flanking sequences. The polynucleotide sequences can be used in the detection of IDAA polynorphisms, in genome mapping, in physical mapping, in positional cloning of genes, in variety identification and in evaluation of genetic variability within and between plant tissues, populations, cultivars, species and species groups. They may also be used to design hybridization probes for oligonucleotide fingerprinting and library screening and to design primers for microsatellite primed PCR. Microsatellite markers are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plant microsatellite sequence; core repeat sequence; detection; probe; DNA polymorphism; genome mapping; physical mapping; fingerprinting; variety identification; genetic variability evaluation; primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1;
                                                                                               Sequence 415 BP;
                                                                                                                                               useful to locate specific economically useful genes in plant genomes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GENE-) GENESIS RES & DEV CORP LTD & FL (FLET-) FLETCHER CHALLENGE FORESTS LTD.
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                      Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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Similarity 72.6%;
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        cgatgaaaatc
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Search completed: September 10, 2002, 21:48:04 Job time: 3296 sec

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